

P65#26 -> Genes
 DNA sequence 1665 b.p. gaattccggcttc ... caagccgaattc linear

P60-1

1	i	gaattccggctcat	ATG	GCG	GCT	AAA	GAC	GTA	AAA	TTC	GTT	GGT	AAC	GAC	GCT	CGT	GTG	AAA	ATG	CTG	CGC	GGC	GTA	AAC	77		
	M	A	A	K	D	V	K	F	N	D	A	R	V	K	M	L	R	G	V	N	21						
22	V	L	A	D	A	V	K	V	T	L	G	P	K	G	R	N	V	V	L	D	K	S	F	G	A	152	
78	GTA	CTG	GCA	GAT	GCA	GTG	AAA	GTT	ACC	CTC	GGC	CCA	AAA	GGC	CGT	AAC	GTA	GTT	CTG	GAT	AAA	TCT	TTC	GGT	GCA	152	
22	V	L	A	D	A	V	K	V	T	S	V	A	R	E	I	E	L	E	D	K	F	E	N	M	G	A	46
153	CCG	ACC	ATC	ACT	AAA	GAT	GGT	GTT	TCC	GTA	GCA	CGT	GAA	ATC	GAA	CTG	GAA	GAC	AAG	TTC	GAA	AAC	ATG	GGT	GCG	227	
47	P	T	I	T	K	D	G	V	S	V	A	R	E	I	E	L	E	D	K	F	E	N	M	G	A	71	
228	CAG	ATG	GTC	AAA	GAA	GTT	GCC	TCT	AAA	GAC	GCG	AAC	GCA	GCT	GCA	GGT	GAC	GGT	ACC	ACC	GCA	ACC	GTA	CTG	GCT	302	
72	Q	M	V	K	E	V	A	S	K	A	N	D	A	A	G	D	G	T	T	A	T	V	L	A	96		
97	Q	S	I	I	T	E	G	L	K	A	V	A	V	A	G	M	N	P	M	D	L	K	R	G	I	121	
303	CAG	TCC	ATC	ATC	GAA	GCC	GGC	CTG	AAA	GCC	GTT	GCT	GCG	GGC	ATG	AAC	CCG	ATG	GAT	CTG	AAA	CGT	GGT	ATC	GAC	377	
122	K	A	V	A	A	V	E	L	K	A	V	A	L	S	V	P	C	S	D	S	K	A	I	A	Q	146	
378	AAA	GCT	GTC	GCT	GCT	GTT	GAA	GAA	CTG	AAA	GCA	CTG	TCC	GTA	CCG	TGC	TCC	GAC	TCT	AAA	GCT	ATT	GCT	CAG	452		
147	V	G	T	I	S	A	N	S	D	E	T	V	G	K	I	A	E	A	M	D	K	V	G	K	171		
453	GTT	GGT	ACC	ATC	TCC	GCT	AAC	TCC	GAC	GAA	ACC	GTA	GGT	AAA	CTG	ATC	GCT	GAA	GCG	ATG	GAC	AAA	GTC	GGT	AAA	527	
172	V	E	G	V	I	T	V	E	D	G	T	G	L	Q	D	E	L	D	V	V	E	G	M	Q	F	D	196
528	GAA	GGC	GTG	ATC	ACC	GTT	GAA	GAC	GGT	ACC	GGT	CTG	CAG	GAC	GAA	CTG	GAC	GTT	GAA	GGT	ATG	CAG	TTC	GAC	602		
197	R	G	Y	L	S	P	Y	F	I	N	K	P	E	T	G	A	V	E	L	E	S	P	F	I	L	221	
603	CGT	GGT	TAC	CTG	TCT	CCT	TAC	TTC	ATC	AAC	AAG	CCG	GAA	ACT	GGC	GCA	GTA	GAA	TTG	GAA	AGC	CCG	TTC	ATC	CTG	677	
222	L	A	D	K	K	I	S	N	I	R	E	M	L	P	V	L	E	A	V	E	A	K	A	G	K	P	246
678	CTG	GCT	GAC	AAG	AAA	ATC	TCC	AAC	ATC	CGC	GAA	ATG	CTG	CCG	GTT	CTG	GAA	GCT	GTA	GCG	AAA	GCA	GGC	AAA	CCG	752	

FIG. 1A

753 CTG CTG ATC ATC GCT GAA GAT GTT GAA GGC GCG CTC GCA ACT CTG GTT GTT AAC ACC ATG CGC GGT ATC GTA 827
 247 L I I D V E A L A T L V V N T M R G I V 271
 828 AAA GTC GCT GCG GTT AAA GCA CCT GGC TTC GGC GAT CGT CGT AAA GCA ATG CTG CAG GAT ATC GCT ACC CTG ACC 902
 272 K V A A V K A P G F G D R R K A M L Q D I A T L T 296
 903 GGT GGT ACC GGT ATC TCT GAA GAG ATC GGT ATG GAG CTG GAA AAA GCA ACT CTG GAA GAT CTG GGC CAG GCG AAA 977
 297 G T V I S E E I G M E L E K A T L E D G V G D E A A I Q G R V 321
 978 CGC GTT ATC AAC AAA GAT ACC ACC ATC ATC GAT GGC GTG GGC GAC GAA GCT GCA ATC CAG GGT CGC GTG 1052
 322 R V I N K D T T I D Y D R E K L Q E R V A K 346
 1053 ACT CAG ATT CGT CAG CAG ATC GAA GAA GCA ACT TCC GAC TAT GAC CGT GAA AAA CTG CAG GAG CGC GTA GCG AAA 1127
 347 T Q I R Q I E A T S D Y D R E K L Q E R V A K 371
 1128 CTG GCA GGC GGC GTT GCG GTT ATC AAA GTT GGT GCG ACT GAA GTT GAA ATG AAA GAG AAG AAA GCC CGC GTT 1202
 372 L A G V A V I K V G A A T E V E M K E K A R V 396
 1203 GAA GAT GCC CTG CAC GCT ACC CGT GCT GCG GTC GAA GAA GGC GTG GTT GCT GGT GGT GGC GTT GCG ATT CGC 1277
 397 E D A L H A T R A V E E G V V A G G V A L I R 421
 1278 GTA GCG TCT AAA ATT GCC GGC CTG AAA GGT CAG AAC GAA GAC CAG AAC GTA GGT ATC AAA GTT GCG CTG CGC GCA 1352
 422 V A S K I A G L K G Q N E D Q N V G I K V A L R A 446
 1353 ATG GAA TCC CCA CTG CGT CAA ATC GTA CTG AAC TGC GGC GAA GAG CCG TCT GTA GTG GCT AAC ACC GTG AAA GCC 1427
 447 M E S P L R Q I V L N C G E E P S V A N T V K A 471
 1428 GGT GAC GGT AAC TAC GGT TAC AAC GCA ACT GAA TAC GCA ACT GAA TAC GGC AAC ATG ATG GGT ATC CTG GAT CCA 1502
 472 G D N Y G Y N A A T E E Y G N M I D M G I L D P 496
 1503 ACC AAA GTA ACT CGT TCT GCT CTG CAG TAC GCG GCT TCT GTC GCG GGT CTG ATG ATC ACC ACC GAG TGC ATG GTT 1577
 497 T K V T R S A L Q Y A A S V A G L M I T T E C M V 521
 1578 ACC GAC CTG CCG AAA GGC GAT GCA CCT GAC TTA GGT GCT GGT GCT GTC GGC GGC ATG GGA ATG ATG TGA 1652
 522 T D L P K G D A P D L G A A G G M G M G M * 546

1653 tcaaggccgaactc

FIG. 1B

P65#44 -> Genes
 DNA sequence 1654 b.p. gaattcggcttc ... aaagccgaattc linear
 use to subclone for expression

P60-2

1	gaattcggctcat	ATG	GCA	AAA	GAA	ATT	AAA	TTT	TCA	TCA	GAT	GCC	CGT	TCA	GCT	ATG	GTC	CGT	GGT	GTC	GAT	ATC	77			
	M	A	K	E	I	K	F	S	S	D	A	R	S	A	M	V	R	G	V	R	G	V	D	I	21	
22	L	A	D	T	V	K	V	T	L	G	P	K	G	R	N	V	L	E	K	S	F	G	S	P	46	
47	L	I	T	N	D	G	V	T	I	A	K	E	I	E	L	E	D	H	F	E	N	M	G	A	K	71
72	L	V	S	E	V	A	S	K	T	N	D	I	A	G	D	G	T	T	A	T	V	L	T	Q	96	
97	A	I	V	R	E	G	I	K	N	V	T	A	G	A	N	P	I	G	I	R	R	G	I	E	T	121
122	A	V	A	A	V	E	A	L	K	N	N	V	I	P	V	A	N	K	E	A	I	A	Q	V	146	
147	A	V	S	S	R	S	E	K	V	G	E	Y	I	S	E	A	M	E	K	V	G	K	D	G	171	
172	V	I	T	I	E	S	R	G	M	E	T	E	L	E	V	V	E	G	M	Q	F	D	R	G	196	
197	Y	L	S	Q	Y	M	V	T	D	S	E	K	M	V	A	D	L	E	N	P	Y	I	L	T	221	
603	TAC	CTT	TCA	CAG	TAC	ATG	GTG	ACA	GAT	AGC	GAA	AAA	ATG	GTG	GCT	GAC	CTT	GAA	AAT	CCG	TAC	ATT	TTG	ATT	ACA	677
678	GAC	AAG	AAA	ATT	TCC	AAT	ATC	CAA	GAA	ATC	TTG	CCA	CTT	TTG	GAA	AGC	ATT	CTC	CAA	AGC	AAT	CGT	CCA	CTC	TTG	752
222	D	K	K	I	S	N	I	Q	E	I	L	P	L	E	S	I	L	Q	S	N	R	P	L	L	246	

FIG. 2A



STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY

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753 ATT ATT GCG GAT GAT GTG GAT GGT GAG GCT CTT CCA ACT CTT GTT TTG AAC AAG ATT CGT GGA ACC TTC AAC GTA 827
 247 I A D D V D G E A L P T L V L N K I R G T F N V 271

 828 GTC GCA GTC AAG GCA CCT GGT TTT GGT GAC CGT CGC AAA GCC ATG CTT GAA GAT ATC GCC ATC TTA ACA GGC GGA 902
 272 V A V K A P G F G D R K A M L E D I A I L T G G 296

 903 ACA GTT ATC ACA GAA GAC CTT GGT CTG GAG TGT AAA GAT GCG ACA ATT GAA GCT CTT GGT CAA GCA GCG AGA GTG 977
 297 T V I T E D L G L E K D A T I E A L G Q A A R V 321

 978 ACC GTG GAC AAA GAT AGC ACG GTT ATT GTA GAA GGT GCA GGA AAT CCT GAA GCG ATT TCT CAC CGT GTT GCG GTT 1052
 322 T V D K D S T V I V E G A G N P E A I S H R V A V 346

 1053 ATC AAG TCT CAA ATC GAA ACT ACA ACT TCT GAA TTT GAC CGT GAA AAA TTG CAA GAA CGC TTG GCC AAA TTG TCA 1127
 347 I K S Q I E T T S E F D R E K L Q E R L A K L S 371

 1128 GGT GGT GTA GCG GTT ATT AAG GTC GGA GCC GCA ACT GAA ACT GAG TTG AAA GAA ATG AAA CTC CGC ATT GAA GAT 1202
 372 G G V A V I K V G A A T E T E L K E M K L R I E D 396

 1203 GCC CTC AAC GCT ACT CGT GCA GCT GTT GAA GGA GGT ATT GTT GCA GGT GGT GGA ACA GCT CTT GCC AAT GTG ATT 1277
 397 A L N A T R A V E G I V A G G T A L A N V I 421

 1278 CCA GCT GTT GCT ACC TTG GAA TTG ACA GGA GAT GAA GCA ACA GGA CGT AAT ATT GTT CTC CGT GCT TTG GAA GAA 1352
 422 P A V A T L E L T G D E A T G D R N I V L R A L E 446

 1353 CCT GTT CGT CAA ATT GCT CAC AAT GCA GGA TTT GAA GGA TCT ATC GTT ATC GAT CGT TTG AAA AAT GCT GAG CTT 1427
 447 P V R Q I A H N A G F E G S I V I D R L K N A E L 471

 1428 GGT ATA GGA TTC AAC GCA ACT GGC GAG TGG GTT AAC ATG ATT GAT CAA GGT ATC ATT GAT CCA GTT AAA GTG 1502
 472 G I G F N A A T G E W V N M I D Q G I I D P V K V 496

 1503 AGT CGT TCA GCC CTA CAA AAT GCA GCA TCT GTA GCC AGC TTG ACA ACA GAA GCA GTC GTA GCC AAT AAA 1577
 497 S R S A L Q N A S V A S L I T E A V V A N K 521

 1578 CCA GAA CCA GTC CCA GCA ATG GAT CCA AGT ATG ATG GGT GGA ATG TGA ccaaggccgaaattc 1654
 522 P E P V A P A M D P S M M D * G M G G G * 542

FIG. 2B



Y65#5 -> Genes
 DNA sequence 1662 b.p. gaattcggcttc ... caagccgaattc linear

Y60-1

1	gaattcggcttcat	ATG	GCG	GCT	AAA	GAT	GTA	AAA	TTC	GGT	AAC	GAC	GCT	CGT	GTA	AAA	ATG	CCT	CGC	GGC	GTA	AAC	77				
1	M	A	A	K	D	V	K	F	G	N	D	A	R	V	K	M	L	R	G	V	N	21					
78	GTA	CTG	GCA	GAC	GCA	GTT	AAA	GTA	ACC	CTG	GGC	CCG	AAA	GGC	CGT	AAC	GTA	GTG	CTG	GAC	AAA	TCC	TTC	GGC	GCG	152	
22	V	L	A	D	A	V	K	V	T	L	G	P	K	G	R	N	V	V	L	D	K	S	F	G	A	46	
153	CCA	ACC	ATC	ACG	AAA	GAT	GGT	GTT	TCT	GTA	GCA	CGT	GAA	ATC	GAG	CTG	GAA	GAC	AAG	TTC	GAA	AAC	ATG	GGC	GCG	227	
47	P	T	I	T	K	D	G	V	S	V	A	R	E	I	E	L	E	D	K	F	E	N	M	G	A	71	
228	CAG	ATG	GTC	AAA	GAA	GTC	GCC	TCT	AAA	GCG	AAC	GAC	GCT	GCA	GGC	GAC	GGT	ACC	ACC	GCG	ACC	GTG	CTG	GCT	302		
72	Q	M	V	W	K	E	V	A	S	K	A	N	D	A	A	G	D	G	T	T	A	T	V	L	A	96	
303	CAG	GCT	ATC	ATC	ACC	GAA	GGT	CTG	AAA	GCC	GTC	GTT	GCT	GCG	GGC	ATG	AAC	CCA	ATG	GAT	CTG	AAA	CGT	GGT	ATC	GAC	377
97	Q	A	I	I	T	E	G	L	K	A	V	A	L	K	A	V	P	M	D	L	K	R	G	I	D	121	
378	AAA	GCT	GTC	GCG	TCC	GCT	GTT	GAA	GAA	CTG	TCC	AAA	GCG	CTG	TCC	GTC	TCT	GAC	TCT	GAC	TCT	AAA	GCC	ATT	GCT	CAG	452
122	K	A	V	S	A	V	E	E	L	K	A	L	K	A	V	P	C	S	D	V	S	D	K	A	I	A	146
453	GTA	GGT	ACC	ATC	TCC	GCT	AAC	TCC	GAC	GAA	ACC	GTA	GGT	AAA	CTG	ATC	GCG	GAA	GCG	ATG	GAT	AAA	GTC	GGT	AAA	527	
147	V	G	T	I	S	A	N	S	D	E	T	V	G	K	L	I	A	E	A	M	D	K	V	G	K	171	
528	GAA	GGC	GTG	ATC	ACC	GTT	GAA	GAC	GGT	ACC	GGT	CTG	GAA	GAC	GAA	CTG	GAC	GTC	GTT	GAA	GGT	ATG	CAG	TTC	GAC	602	
172	E	G	V	I	T	V	E	D	G	T	G	L	E	D	V	V	E	G	M	Q	F	D	V	E	L	196	
603	CGC	GGT	TAC	CTG	TCC	CCA	TAC	TTC	ATC	AAC	AAG	CCA	GAA	ACT	GGC	GCT	GTT	GAG	CTG	GAA	AGC	CCG	TTC	ATC	CTG	677	
197	R	G	Y	L	S	P	Y	F	I	N	K	P	E	T	G	A	V	E	L	E	S	P	F	I	L	221	
678	CTG	GCT	GAC	AAG	AAA	ATC	TCC	AAC	ATC	CGC	GAA	ATG	CTG	CCA	GTG	CTG	GAA	GCC	GTT	GCG	AAA	GCA	GGC	AAA	CCG	752	
222	L	A	D	K	I	S	N	I	R	E	M	L	P	V	L	E	A	V	A	K	A	G	K	P	246		

FIG. 3A



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753	CTG	GTT	ATC	ATT	GCT	GAA	GAC	GTT	GAA	GCG	CTG	GCG	ACC	CTG	GTT	AAC	ACC	ATG	CGT	GGC	ATC	GTG	827				
247	L	V	I	A	E	D	V	E	G	E	A	T	L	V	N	T	M	R	G	I	G	I	V	271			
828	AAA	GTC	GCT	GCG	GTC	GTT	AAA	GCA	CCT	GCG	GAC	GGC	CGT	AAA	GCG	ATG	CTG	CAG	GAT	ATC	GCT	ACC	CTG	ACC	902		
272	K	V	A	V	K	A	P	G	F	D	R	R	K	A	M	L	Q	D	I	A	T	L	T	T	296		
903	GGC	GTC	GGT	ACC	GTC	ATC	TCT	GAA	GAG	ATG	GAG	CTG	GAA	AAA	GCG	ACC	CTG	GAA	GAC	CTG	GGC	CAG	GCT	AAA	977		
297	G	G	T	V	I	S	E	E	G	M	E	L	E	K	A	T	L	E	D	L	G	Q	A	K	321		
978	CGT	GTT	GTG	ATC	AAC	AAA	GAC	ACC	ACC	ATC	ATC	GAT	GGC	GTG	GGC	GAC	GAA	GCG	GCG	ATT	CAG	GGC	CGT	GTG	1052		
322	R	V	V	I	N	K	D	T	T	I	I	D	G	V	G	D	E	A	I	A	I	Q	G	R	V	346	
1053	GGT	CAG	ATC	CGT	AAC	AAG	CAG	ATC	GAA	GAA	GCC	ACT	TCC	GAT	TAC	GAC	CGT	GAA	AAA	CTG	CAG	GAG	CGC	GTA	GCG	AAA	1127
347	G	Q	I	R	K	Q	I	E	E	A	T	S	D	Y	D	R	E	K	L	Q	E	R	V	A	K	371	
1128	CTG	GCA	GGC	GGT	GGT	GTT	GCG	GTC	AAA	GTC	GCT	GCG	ACT	GAA	GTT	GAA	ATG	AAA	GAG	AAA	AAA	GCA	CGC	GTG	1202		
372	L	A	G	G	V	A	V	I	K	V	G	A	A	V	E	M	K	E	K	E	M	K	A	R	V	396	
1203	GAC	GAT	GCC	CTG	CAC	GCG	ACC	CGT	GCT	GCG	GTC	GAA	GAA	GGA	GGC	GTG	GTT	GCT	GCT	GCT	GCT	GCG	CTG	GTG	CGT	1277	
397	D	D	A	L	H	A	T	R	A	V	E	E	G	V	V	A	G	G	G	V	A	L	V	R	A	421	
1278	GTT	GCC	GCG	AAA	CTG	TCC	GCG	CTG	ACT	GCT	GCG	CAG	AAC	GAA	GAT	CAG	AAC	GTC	AAA	GTT	GCG	CTG	CGC	GCA	1352		
422	V	A	A	K	L	S	G	L	T	A	Q	N	E	D	Q	N	V	G	I	K	V	A	L	R	A	446	
1353	ATG	GAA	GCT	CCA	CTG	CGT	CAG	ATC	GTC	TCC	AAC	GCC	GGT	GAA	GAG	CCA	TCT	GTT	GTG	ACC	AAC	ATG	AAA	GCA	1427		
447	M	E	A	P	L	R	Q	I	V	S	N	A	G	E	E	P	S	V	T	N	N	V	K	A	471		
1428	GGC	GAA	GGT	AAC	TAC	GGT	TAC	AAC	GCA	GCA	ACT	GAA	TAC	GGC	AAC	ATG	ATC	GAC	TTC	GGT	ATC	CTG	GAT	CCA	1502		
472	G	E	G	N	Y	G	Y	N	A	A	T	E	E	Y	G	N	M	I	D	F	G	I	L	D	P	496	
1503	ACC	AAA	GTG	ACC	CGT	TCT	GCT	CTG	CAG	TAC	GCG	GCA	TCT	GTC	GCT	GGC	CTG	ATG	ATC	ACC	ACC	GAG	TGC	ATG	GTG	1577	
497	T	K	V	T	R	S	A	L	Q	Y	A	A	S	V	A	G	L	M	I	T	T	E	C	M	V	521	
1578	ACC	GAC	CTG	CCT	AAA	GGC	GAC	GCA	CCT	GAC	TTA	GGT	GCT	GCA	GGC	ATG	GGT	GGT	ATG	ATG	TGA	tcaa	1653				
522	T	D	L	P	K	G	D	A	P	D	L	G	A	A	G	M	G	G	M	G	M	M	*	545			

1662

FIG. 3B

1654 gcccgaattc



Y65#21 -> Genes
 DNA sequence 1661 b.p. gaattcggtttc ... TAAggccaaatcc linear
 V261 - same in clone Y65#24, too
 used to subclone for expression !!!

Y60-2

1	gaattcggtttcat	ATG	GCA	AAA	GAA	ATC	AAA	TTT	TCA	GCA	GAT	GCG	CGT	GCT	GCC	ATG	GTC	GCG	GGA	GTT	GAT	ATG	77				
	M	A	K	E	I	K	F	S	A	D	A	R	A	M	V	R	G	V	R	G	V	D	M	21			
22	L	A	D	T	V	K	V	T	L	G	P	K	G	R	N	V	V	L	E	K	A	F	G	46			
153	L	I	T	N	D	G	V	T	I	A	K	E	I	E	L	E	D	H	F	E	N	M	G	71			
47	228	TTC	GTC	TCT	GAA	GTG	GCT	TCT	AAA	ACC	AAT	GAT	ATT	GCT	GGT	GAT	GGG	ACG	ACT	ACT	GCA	ACA	GTT	TTG	ACA	CAA	302
72	L	V	S	E	V	A	S	K	T	N	D	I	A	G	D	G	T	T	A	T	V	L	T	Q	96		
303	97	GCC	ATT	GTT	CAT	GAA	GGG	CTA	AAA	AAAT	GTG	ACA	GCA	GGT	GCT	AAT	CCA	ATT	GGT	ATC	CGT	CGA	GGC	ATT	GAA	ACA	377
	A	I	V	H	E	G	L	K	N	V	T	A	G	A	N	P	I	G	I	R	R	G	I	E	T	121	
378	122	GCA	ACA	GCA	ACA	GCT	GTT	GAA	GGG	TTC	AAA	GCC	ATT	GCT	CAA	CCT	GTA	TCT	GGC	AAG	GAA	GCT	ATT	GCT	CAG	GTC	452
	A	T	A	T	A	V	E	A	L	K	A	I	A	Q	P	V	S	G	K	E	A	I	A	Q	V	146	
453	147	GCT	GCA	GTA	TCA	TCA	CGC	TCT	GAA	AAA	GTT	GGG	GAG	TAT	ATC	TCA	GAA	GCT	ATG	GAG	CGT	GTG	GGC	AAC	GAT	GTC	527
	A	V	S	S	R	S	E	K	V	G	E	Y	I	S	E	A	M	E	R	V	G	N	D	G	171		
528	172	GTC	ATT	ACC	ATC	GAA	GAA	TCT	CGA	GGT	ATG	GAA	GAA	CTT	GAA	GTG	GTT	GAA	GGC	ATG	CAA	TTT	GAC	CGT	CGT	602	
	V	I	T	I	E	S	R	G	M	E	T	E	L	E	V	V	E	G	M	Q	F	D	R	G	196		
603	197	TAC	CTG	TCT	CAA	TAC	ATG	GTC	ACA	GAC	AAT	GAA	AAA	ATG	GTC	GAC	CTT	GAA	AAC	CCA	TTT	ATC	ATC	ACG	677		
	Y	L	S	Q	Y	M	V	T	D	N	E	K	M	V	A	D	L	E	N	P	F	I	L	I	T	221	
678	222	GAT	AAA	AAA	GTG	TCA	AAC	ATC	CAA	GAC	ATT	TTG	CCA	CTA	CTT	GAG	GAA	GTT	CTT	AAA	ACC	AAC	CGT	CCA	TTA	CTC	752
	D	K	K	V	S	N	I	Q	D	I	L	P	L	E	E	V	L	E	E	N	R	T	N	R	P	L	246

FIG. 4A

753 ATT ATT GCA GAT GAT GTG GAT GGT GAA GCA CTT CCA ACC CTT GTC TTG AAC AAG ATT CGT GGT ACT TTC AAT GTG 827
 247 I I A D D V D P L N K I R G T F N V 271

 828 GTT GCT GTC AAA GCG CCA GGA TTT GGT GAT CGT CGT AAA GCT ATG CTT GAA GAC ATT GCT ATC TTG ACA GGT GGT 902
 272 V A V K A P G F G D R R K A M L E D I A I L T G G 296

 903 ACA GTG ATT ACA GAG GAT CTA GGA CTT GAA TTA AAA GAT GCT ACA ATG ACA GCC CTT GGA CAG GCT GCT AAG ATT 977
 297 T V I T E D L G L E L K D A T M T A L G Q A A K I 321

 978 ACA GTT GAT AAA GAT AGC ACA GTA ATT GTT GAA GGT TCA GGA AGT TCA GAA GCT ATT GCT AAC CGT ATT GCA CTG 1052
 322 T V D K S T V I V E G S S G S E A I A N R I A L 346

 1053 ATT AAA TCG CAA TTA GAA ACA ACT TCT GAC TTT GAC CGT GAA AAA CTA CAA GAA CGT TTG GCG AAA TTA GCT 1127
 347 I K S Q L E T T S D F D R E K L Q E R L A K L A 371

 1128 GGT GGT GTA GCT GTT ATC AAA GAA ATA GCA GCT CCA ACA GAG ACA GCT TTA AAA GAA ATG AAA CTT CGC ATT GAG GAT 1202
 372 G G V A V I K V G A P T E T A L K E M K L R I E D 396

 1203 GCT CTA AAT GCT ACA CGT GCA GCC GTT GAA GAA GGT ATC GTT GCT GGT GGA ACA GCA CTT ATT ACG GTT ATT 1277
 397 A L N A T R A V E E G I V A G G T A L A L T V I 421

 1278 GAA AAA GTA GCA GCT CTT GAG CTT GAG GGC GAT GAT GCT ACT GGA CGT AAC ATT GTG CTT CGT GCT CTA GAA GAG 1352
 422 E K V A A L E G D D A T G R N I V L R A L E E 446

 1353 CCT GTA CGT CAA ATT GCT TTA AAT GCT GGG TAC GAA GGC TCC GTA GTT ATT GAC AAG TTG AAA AAC AGC CCT GCA 1427
 447 P V R Q I A L N A G Y E G S V V I D K L K N S P A 471

 1428 GGA ACA GGA TTT AAT GCT GCA ACA GGT GAG TGG GTT GAT ATG ATT AAA ACA GGA ATC ATT GAC CCT GTC AAA GTA 1502
 472 G T G F N A A T G E W V D M I K T G I I D P V K V 496

 1503 ACA CGA TCA GCG CTT CAA AAT GCA GCT TCT GTA GCT AGT CTT ATT TTG ACA ACA GAA GCA GTT GCT AAT AAA 1577
 497 T R S A L Q N A A S V A S L I L T T E A V V A N K 521

 1578 CCT GAA CCA GCT ACG CCA GCG CCA GCA ATG CCA GGA GGT ATG GAT CCA GGA ATG ATG GGT GGG ATG GGC GGA TAA 1652
 522 P E P A T P A M P A G M D P G M M G G 6 M G 6 G △ 546

1653 gccgaattc

FIG. 4B



Sequencing strategy (scale : 1cm = approx. 100bp)

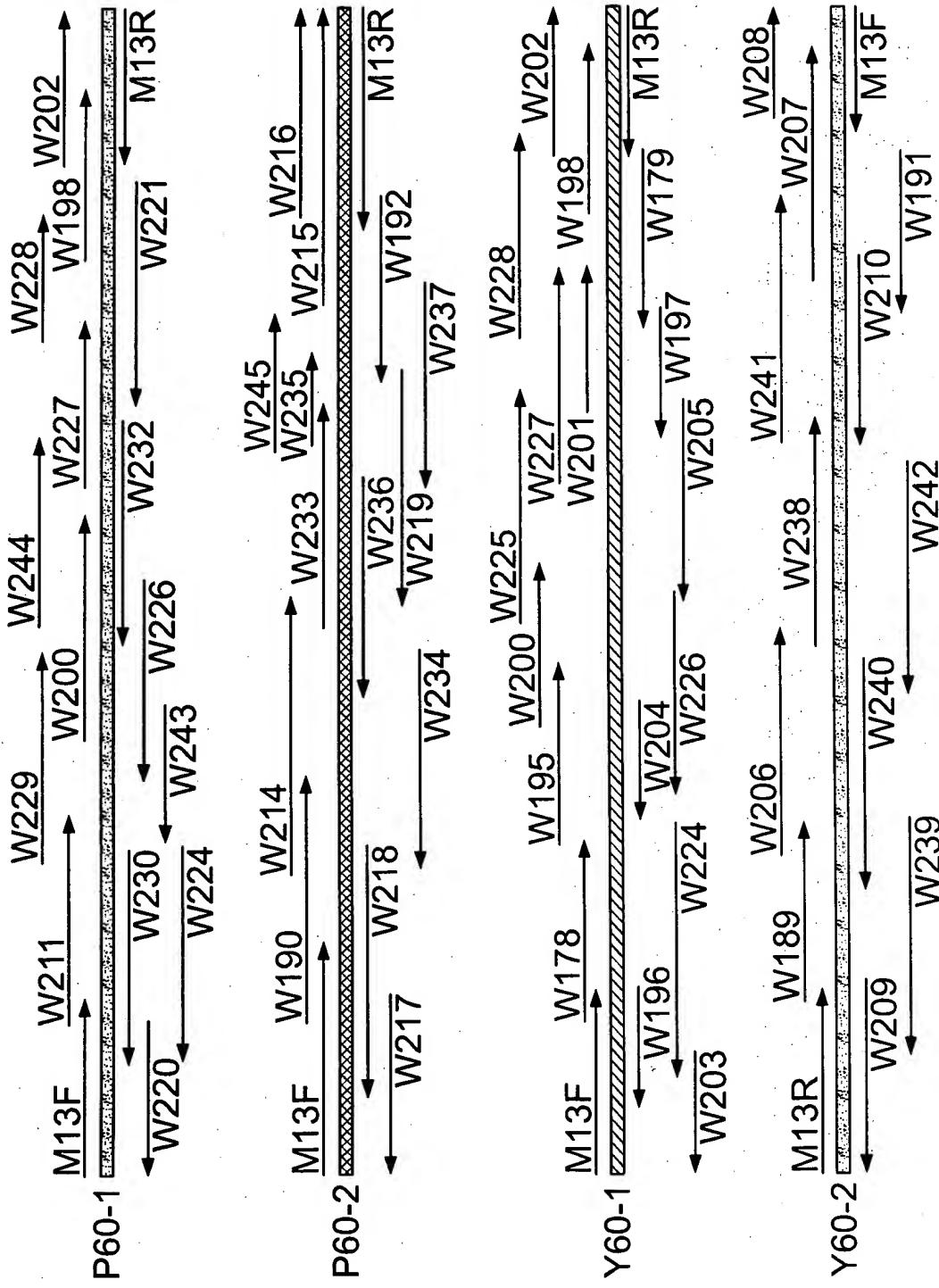
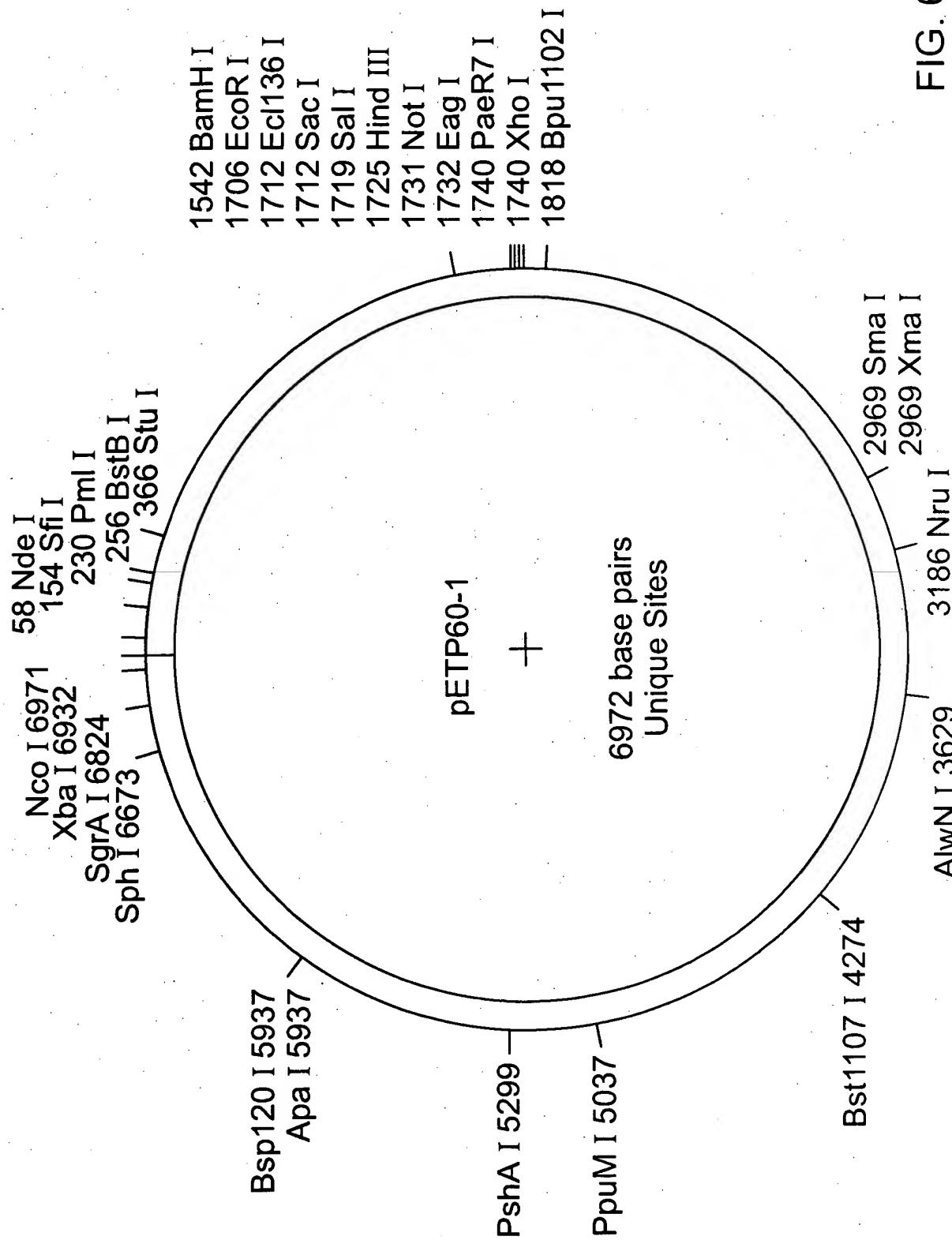


FIG. 5



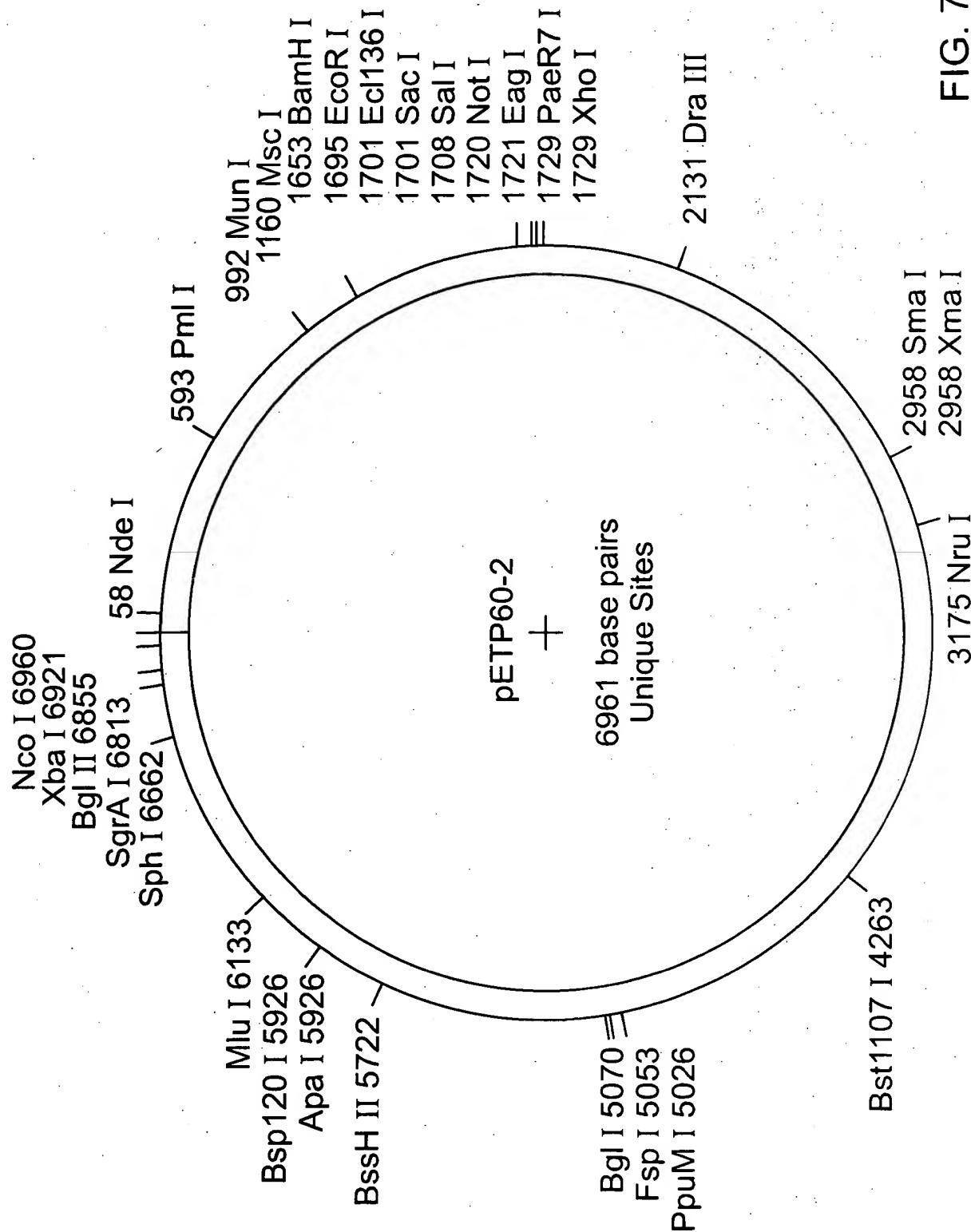


FIG. 7

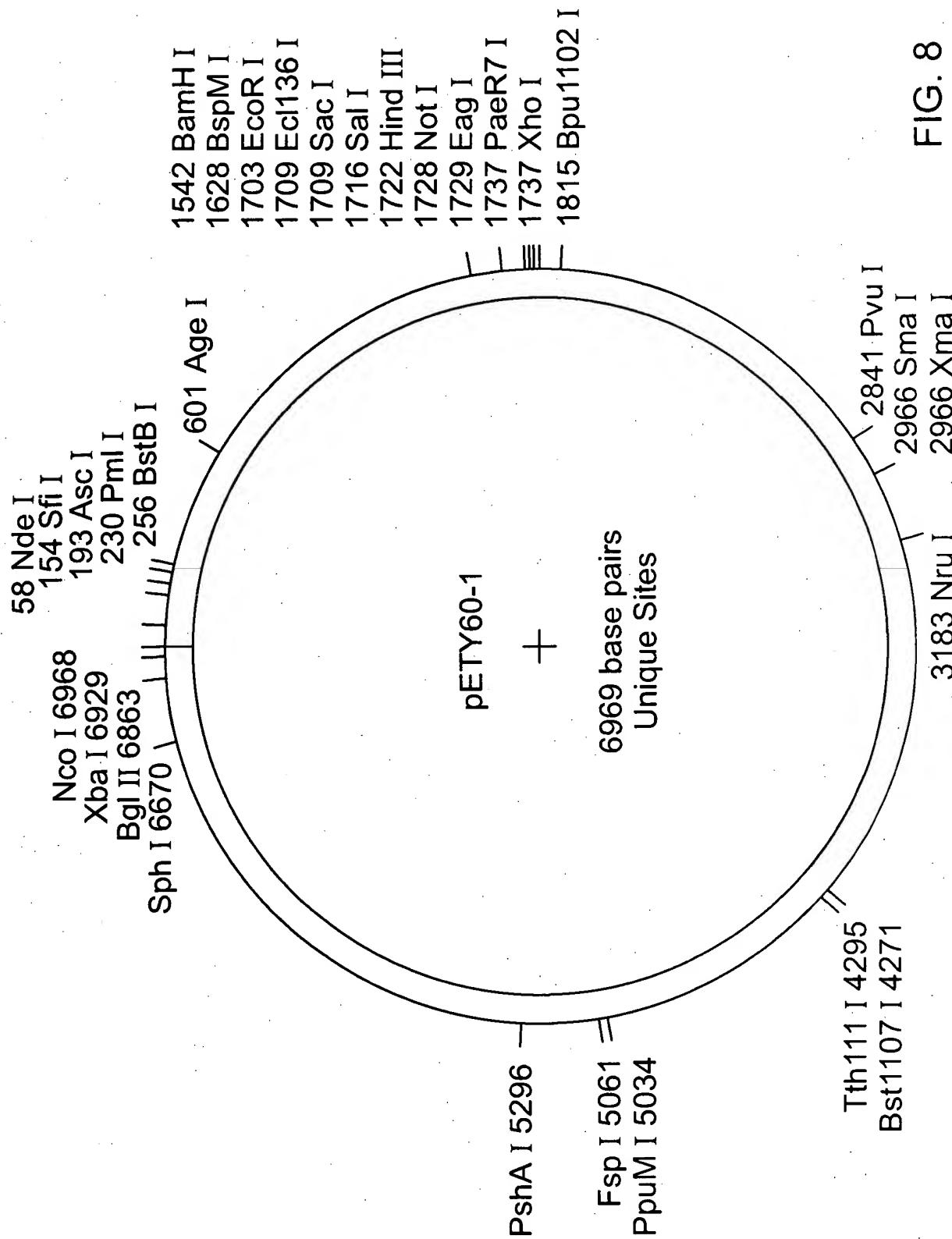


FIG. 8

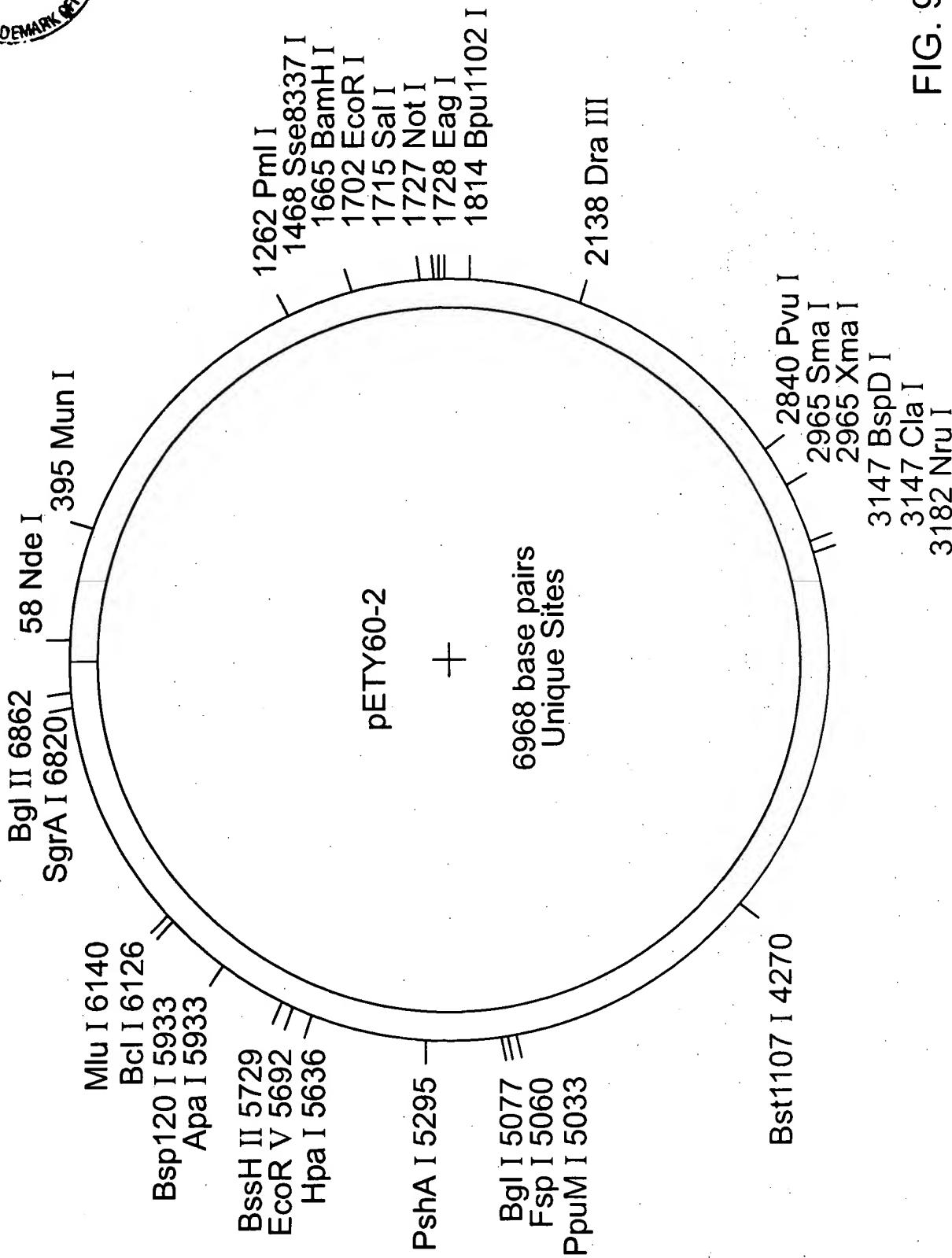


FIG. 9



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 STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY
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 09/001,737
 12071-014001

MA-----	10	20	30	40	50	60	70	80	90	100	110	120	130
<i>S. pneumoniae</i> MA-----													
<i>S. pyogenes</i> hs MA-----													
<i>S. pneumoniae</i> MA-----													
<i>S. pyogenes</i> hs MA-----													
<i>B. subtilis</i> gr MA-----													
<i>Clostridium</i> h MA-----													
<i>Cowdria</i> hsp60 MA-----													
<i>Haemophilus</i> h MA-----													
<i>L. pneumophila</i> MA-----													
<i>M. avium</i> hsp60 MA-----													
<i>M. bovis</i> hsp60 MA-----													
<i>M. leprae</i> groe MS-----													
<i>M. leprae</i> hsp6 MA-----													
<i>M. tuberculosis</i> MS-----													
<i>N. meningitidis</i> MA-----													
<i>S. aureus</i> hsp6 MV-----													
<i>Synechocystis</i> MA-----													
<i>Synechocystis</i> MS-----													
<i>Tsukamurella</i> MA-----													
<i>S. pombe</i> hsp60 M-----													
<i>S. cerevisiae</i> M-----													
<i>P. falciparum</i> M-----													
<i>Oncocerca</i> hs MTN-----													
<i>C. elegans</i> hsp M-----													
<i>D. melanogaster</i> M-----													
human hsp60 M-----													
Arabidopsis h M-----													
maize hsp60 M-----													
RUBISCO chaperon M-----													
MASTNA LSLSLRSPTNQAQTSLSKKVQHGRNFRRKPNRFVKAAKDIAFDQHSRSAMQIDKLADAVGLTLGPRGRNVLD-EFGSPKVNDGVTTARATELPDMENAGAIIREVASKTND 129													

--KDKFGEFARRMLRGVNAALADAVKVTLGPKGRNVWLEKSGAPTTKGVTVAKEIELEDKFENMGAGLVKEYASKTNDV

--AKDVKFGNDARVKMLRGVNVLADAVKVTLGPKGRNVWLEKSGAPTTKGVTVAKEIELEDKFENMGAGLVKEYASKTNDV 84

--AKDVKFGNDARVKMLRGVNVLADAVKVTLGPKGRNVWLEKSGAPTTKGVTVAKEIELEDKFENMGAGLVKEYASKTNDV 84

--KEIKFSSDARSANWRGVDLADTVKVLGPKGRNVWLEKSGAPTTKGVTVAKEIELEDKFENMGAGLVKEYASKTNDV 83

--KEIKFSSDARSANWRGVDLADTVKVLGPKGRNVWLEKSGAPTTKGVTVAKEIELEDKFENMGAGLVKEYASKTNDV 83

--KEIKFSEFARRMLRGVDAALADAVKVTLGPKGRNVWLEKSGAPTTKGVTVAKEIELEDKFENMGAGLVKEYASKTNDV 83

--KTLFGEFARRMSAQGVQLANTVCKTLGPKGRNVWLEKWFQAPTNTDGVTVAKEIELEDYEMGQLVKEYASKTNDV 83

--VVTGEQDOKSREWRVLEDAVNGCTAGPKGTLVATSPYGAPEVTKQGTLVAKDVKLNGVNLQASQMDK 83

--AKDVKFGNDARVKMLRGVNVLADAVKVTLGPKGRNVWLEKSGAPTTKGVTVAKEIELEDKFENMGAGLVKEYASKTNDV 84

--KELRGDDARLQLMAGVNAALADAVQTMGPRGRNVWLESYGAPTVTKQGVSVAKEIEEFHRFMGMQVNKEVASKTSD 83

--KTIAYDEEARRGLERGLINALADAVKVTLGPKGRNVWLEKWFQAPTNTDGVTVAKEIELEDYKIGAEILVKEVAKKTDDV 83

--KTIAYDEEARRGLERGLINALADAVKVTLGPKGRNVWLEKWFQAPTNTDGVTVAKEIELEDYKIGAEILVKEVAKKTDDV 83

--KLEYDETARHAMEVMNKLADEVKVTTLGPRGRNVWLEKWFQAPTNTDGVTVAKEIELEDYKIGAEILVKEVAKKTDDV 83

--KTIAYDEEARRGLERGLNSLADAVKVTLGPKGRNVWLEKWFQAPTNTDGVTVAKEIELEDYKIGAEILVKEVAKKTDDV 83

--KLIYEYDETARRAMEVMNKLADEVKVTTLGPRGRNVWLEKWFQAPTNTDGVTVAKEIELEDYKIGAEILVKEVAKKTDDV 83

--AKDVOFGNEVROKMWNGVNLTANARVTLGPKGRNVVDRAGFQPHITKQGVSVLAKDFTAPLTDNGVTVAKEIELEDYEMGAKLQEVAKNTNEI 84

--KOLKFSEDARQAMLRGVDQQLANAVKVTIGPKGRNVLDEKFGSPQTLNGDTTAKEIELEDYEMGAKLQEVAKNTNEI 83

--KSLIYNDEARRALERGMDLADEVAVTLGPKGRNVWLEKWFQAPTNTDGVTVAKEIELEDYEMGAKLQEVAKNTNEI 83

--KLSFKDERSRSLEAGINALADAVRJLGPGRNVLLEKYQGAPOLNDGVTVAKEIELNPEENAGAKLQEVAKTEI 83

--KTAIFDKKARRGLERGLINALADAVKVTLGPKGRNVLLEKWFQAPTNTDGVTVAKEIELEDYKIGAEILVKEVAKKTDDV 83

--A--KDKFGDVDRASLLTGVDTLARAISVTLGPKGRNVLIDOPFGSPKITKDGTWTGQVSI GARLQDVIAVSKTNE 115

--S--SHKELKFGEVERBASLKGVETLADEVAVTLGPKGRNVLI EQFGPPKPKITKDGTWTGQVSI VLGKFFENMGAKLQEVAKNTNEA 108

--I--S--KDIRFGSDRTAMITGCNKLADAVSYTLGPKGRNVII EQSFSGSPKITKDGTWTGQVSI EFNFKLANI GAQMVQVAANTNGK 113

--VWSGEQLOQAFREVAVIDSTAVTAGPKGVIGI NKPYGAPEITKDGTVMKGJ KPEKPLNAAITSIFAQSCSQCDK 83

--LQAVWVS Y--A--KDKFGAEGRQAMLYGVNVLLADAVSUTMGPGRNVII EQSGSGSPKITKDGTWTGQVSI DQVANKANE 99

--RKG--LA--MRG--Y--A--KDVRFGPETRAMI QGDVII ADAIVATMGPGRNVII EQSGSGSPKITKDGTWTGQVSI DQVLANNTNEE 104

--FRLPSL--ARSSISRQ--LA--MRG--Y--A--KDKFGADARMLKGVDLADAVATMGPGRNVII EQSGSGSPKITKDGTWTGQVSI DQVANNTNEE 108

--LRLPTVFROMPNSRV--LAPHLTRA--Y--A--KDKFGADARMLKGVDLADAVATMGPGRNVII EQSGSGSPKITKDGTWTGQVSI DQVANNTNEE 108

--ARQVSS--RMSWSRN--Y--AA--KEIKFGEVERAALMLKGVDLADAVATMGPGRNVII EQSGSGSPKITKDGTWTGQVSI DQVANNTNEE 114

--YRFASNLASKARIQN--RFLAWSRN--Y--AA--KDKFGADARMLKGVDLADAVATMGPGRNVII EQSGSGSPKITKDGTWTGQVANAINDN 117

FIG. 10A

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 STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY

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	140	150	160	170	180	190	200	210	220	230	240	250	260
<i>S. pneumoniae</i>	AGDGTATVLAQATIVKEGLKNVAAGANPMDLRGGIDKAVDAVEELKATAKPV--ETKEEIAQVATISANGDEEIGE---LIAEAMEVKGKEGVITV---EEGKTLETLEVEG-MQFDRGYISYPFI												
<i>S. pyogenes</i> hs	AGDGTATVLAQATIVKEGLKNVAAGANPMDLRGGIDKAVDAVEELKATAKPV--SDSKATAQVGTSANSDETYIK---LIAEAMDKVKGKEGVITV---EDGTGQDELDWEG-MQFDRGYISYPFI	205											
<i>S. pneumoniae</i>	AGDGTATVLAQATIVREGTKNVTAGANPIGIRGTTAIVAAVEALKNNVTPV--ANKEATAQVAVASS-RSEKIGE---YISEAMEVKGDGVITI---EESRGMELEWEG-MQFDRGYLSQYMF	203											
<i>S. pyogenes</i> hs	AGDGTATVTLQATIVHEGLKNVTAGANPIGIRGTTAIVAAVEALKNNVTPV--SKEATAQVAVASS-RSEKIGE---YISEAMEVRGNDGVITI---EESRGMELEWEG-MQFDRGYLSQYMF	203											
<i>B. subtilis</i> gr	AGDGTATVLAQAMIREGLKNVTAGANPIGVRKGMEQAVAVATENKEISKPI--EGKESTAQVAAISA-ADEEVGS--LIAEAMERVGNDGVITI---EESKGFTTELEWEG-MQFDRGYASPYMF	203											
<i>C. Crostidium</i> h	AGDGTATVLLAQATITREGLKNVTAGANPLIIRNGTKTAKAVEKAVEETQKTSKPV--NGKEDTARVAISA-ADEKIGK---LIAEAMDKVKGKEGVITV---EESKGFTTELEWEG-MQFDRGYVSAYMF	203											
<i>C. Crostidium</i> h	VGDGTTCISLTAKVIEVSKVKAAGADTICVREGIKAKAEVALNEAKLCKMREVLSE--EEIAQVATISANGDKNTGK---EETKEQVGTISANSSTVQG---LIAQCYKEVGKDGTVVEESKGFKEL--DVEKTDG-MQFDRGYLSYPFI	205											
<i>Haemophilus</i> h	AGDGTATVTLQATIVNEGLKAVAAAGMNPMDLRGGIDKAVDAVEELKATAKPV--ETSKETEIQVGTISANSSTVQG---LIAQCYKEVGKDGTVVEESKGFKEL--DVEKTDG-MQFDRGYLSYPFI	205											
<i>L. pneumophili</i> 1a	AGDGTATVTLQATIVLARSILVEGHKAVAAAGMNPMDLRGGIDKAVDAVTLKKLQAMSXTC--KDSKATAQVGTSANSDFATIGA---LIAEAMEVKGKEGVITV---EDGNGLENELSVEG-MQFDRGYISYPFI	204											
<i>M. avium</i> hsp60	AGDGTATVTLQALVREGLRMVAAGANPLGLKRGFIEKAVEKVTETLLSAKEV--ETKDQJATAAISA-GDQ51GD--LIAEAMDKVKGMEGVITV---EESNTTGLQLELTEG-MRFDKGYSQYFV	203											
<i>M. bovis</i> hsp60	AGDGTATVTLQALVREGLRNAVAGANPLGLKRGFIEKAVEKVTETLLGAKEV--ETKEQJAAIAISA-GDQ51GD---LIAEAMDKVKGMEGVITV---EESNTTGLQLELTEG-MRFDKGYSQYFV	203											
<i>M. leprae</i> groE	AGDGTATVTLQALVREGLKGGLRVAAGANPLGLKRGFIEKAVEKVTETLLSAKEV--AGKDAITQVATVSSR-DEQ1GA--LVGEAMKVGKDGTVVSV---EESNTTGLQLELTEG-MRFDKGYSQYFV	203											
<i>M. leprae</i> hsp6	AGDGTATVTLQALVREGLKGGLRVAAGANPLGLKRGFIEKAVEKVTETLLSAKEV--ETKEQJAAIAISA-GDQ51GD---LIAEAMDKVKGMEGVITV---EESNTTGLQLELTEG-MRFDKGYSQYFV	203											
<i>M. tuberculosis</i>	AGDGTATVTLQALVREGLKGGLRVAAGANPLGLKRGFIEKAVEKVTETLLSAKEV--SIGHTIAQVATVSSR-DEQ1GD--LVGEAMSKVGKDGTVVSV---EESNTTGLQLELTEG-MRFDKGYSQYFV	203											
<i>N. meningitidis</i>	AGDGTATVTLQASVIAEGKYYTAGMNPDLRGKIDKAVAAVLEEKNTAKPC--DTSKETAQVGTSISANSDEQGA--LIAEAMEVKGKEGVITV---EDGKSUENEELDVVEG-MQFDRGYISYPFI	205											
<i>S. aureus</i>	AGDGTATVTLQALMQUEGLRNVTAQVAKVAVAEHANNSOKPV--ENKEIAQVGTISANGDKNTGK---LIAEAMDKVKGMEGVITV---EESNTTGLQLELTEG-MRFDKGYSQYFV	204											
<i>Synechocystis</i>	AGDGTATVTLQALVREGLKNVAAGANPLGLKRGFIEKAVETFLVQEAEAKPV--GDSKATAQVATVSSGNDPEVGA--MIADANDKVTQDGTVV---EESKSINTLEWEG-MQIDRGYISYPFI	203											
<i>T. sakamurei</i> 1a	AGDGTATVTLQALVREGLKNVAAGANPLGLKRGFIEKAVETEHLKKAAKEV--ETKDQJAAATAGISA-GDP41GE--LIAEAMEVKGKEGVITV---EESNTTGLQLELTEG-MRFDKGYSQYFV	203											
<i>S. pombe</i> hsp60	AGDGTATVTLRAIFSETVNRVAAGCNPMDLRGGIDKAVDAVNLWEEFLQANRKDI--TTSEETISQVATISANGDTIGE---LLAKAMERVGKEGVITV---KEGRITSDELEVENTEG-MKFDRGYISYPFI	236											
<i>S. cerevisiae</i>	AGDGTATVTLQALMQUEGLRNVTAQVAKVAVAEHANNSOKPV--TTSEEIAQVATISANGDKNTGK---LLASAMIEVKGREGVITI---REGRTLSDELEVENTEG-MRFDGFISYPFI	226											
<i>P. falci parum</i>	AGDGTATVTLRSIFQQGKAVDSGMNPMDLRGGIDKAVDAVNLWEEFLQANRKDVLEIINSIKKD---TTTEETENVAVATIS-NGDKNTGQ---LIADTMKVKGREGVITI---TEGTLQHELEVIEG-MKFDRGYISYPFI	233											
<i>Onchocerca</i> hs	VGDGTTCCTSLTSGMVEASKSTAAGNDRISIISKMGQAKDVVLKEVASMARTISELKIDEVAQVATISANGDRSISGN---IADAWMKVKGREGVITVVEESGSKEL--EVELTITG-MQFDRGYLSYPFI	207											
<i>C. elegans</i> hsp	AGDGTATVTLRAIKAIFERHSSRGNAYAEIRGMMAVEWVAEKKLSSKV--TTPEEIAQVATISANGDTIGE---LISDANKVKGREGVITV---KOGKTUNDQLELTEG-MKFDRGYISYPFI	220											
<i>D. melanogaster</i>	AGDGTATVTLRAIKAEGFEKISKGPNPIERGGWMLAVETVDKDNLKTMSPV--SPPTEETQVATISANGDREIINGKYSVEANKKVKGREGVITV---KOGKTUNDQLELTEG-MKFDRGYISYPFI	229											
human hsp60	AGDGTATVTLRAIKAEGFEKISKGPNPIERGGWMLAVETVDKDNLKTMSPV--TTPEEIAQVATISANGDTIGE---LISDANKVKGREGVITV---KOGKTUNDQLELTEG-MKFDRGYISYPFI	229											
Arabidopsis h	AGDGTATCATTWKTAIFTEGCKSVAAGMNAANDLRGGISMAVDAVTNLKGARMII--STSEEIAQVGTISANGEREIGE---LIAKAMEVKGKEGVITI---ADGNTLYNELEWEG-MKLDRGYISYPFI	238											
maize hsp60	AGDGTATCATTWKTAIFTEGCKSVAAGMNAANDLRGGISMAVDAVTNLKGARMII--STSEEIAQVGTISANGEREIGE---LIAKAMEVKGKEGVITI---ADGNTLYNELEWEG-MKLDRGYISYPFI	238											
RUBISCO chaperon	AGDGTATVTLRAIKAEGFEKISKGPNPIERGGWMLAVETVDKDNLKTMSPV--KGGDDIKAVATISAGNDLIGK---MIAEAIDKVAATISAGNDLIGK---ESSNSFETTVEEGLPQLSI---ESSNSFETTVEEGLPQLSI	250											

FIG. 10B



TDSEIQQKAAELEDPLILLTQDKISNQDILLPVLEVA--	QAGKPLLIIDAEDEGEALATLVNKLRGTLKVIVAVKAPGFDRRKAMILDIAITLTGGVISEE-LG	LSLEDAITED-LGQAKKVWVTKDTT	
	300	310	320
	290	300	310
	280	290	300
	270		

S. pneumoniae NKPETGAVELESPFILLADKKISNIREMPLPLEVA--KAGKPLLIIDAEDEGEALATLVNKLRGTLKVIVAVKAPGFDRRKAMILDIAITLTGGVISEE-LGMEKATED-LGQAKRVWINKDTT
S. pyogenes has NKPETGAVELESPFILLADKKISNIREMPLPLEVA--KAGKPLLIIDAEDEGEALATLVNKLRGTLKVIVAVKAPGFDRRKAMILDIAITLTGGVISEE-LGMEKATED-LGQAKRVWINKDTT 331
S. pneumoniae TDSEKMKVADLENPFYLTDKKISNQELIPPLESTL--QSMPRLPLIADDDGEALPTLVNKIRGTFTIVVAVKAPGFDRRKAMILDIAITLTGGVISEE-LGMEKATED-LGQAKRVWINKDTT 331
S. pyogenes has TDSEKMKVADLENPFYLTDKKISNQELIPPLEEVIL--KTMRPLPLIADDDGEALPTLVNKIRGTFTIVVAVKAPGFDRRKAMILDIAITLTGGVISEE-LGMEKATED-LGQAKRVWINKDTT 329
B. subtilis gr. TDSDRMEAVLDNPYPLITDKKISNQELIPPLEQIV--QQGKPLLIIDAEDEGEALPTLVNKIRGTFTIVVAVKAPGFDRRKAMILDIAITLTGGVISEE-LGMEKATED-LGQAKRVWINKDTT 329
Clostridium h TDTERMEAVLDNPYPLITDKKISNQELIPPLEQIV--QAGKPLLIIDAEDEGEALPTLVNKIRGTFTIVVAVKAPGFDRRKAMILDIAITLTGGVISEE-LGMEKATED-LGQAKRVWINKDTT 329
Cordria hsp60 TNSERMLVIEFNPYILLTEKKLNIIQPLPLPENTA--RSGRPLLIIDAEDEGEALSTLVNLKLRGGLHVAVKAPGFDRRKAMILDIAITLTGGVISEE-LGMEKATED-LGQAKRVWINKDTT 332
Haemophilus h NKPETATVELDNPFPILLWDKKISNIRELPVLEGIA--KAGKPLLIIDAEDEGEALATLVNNMRGTVKIVAVKAPGFDRRKAMILDIAITLTGGVISEE-LGMEKATED-LGQAKRVWINKDTT 331
L. pneumophila NNQNMNSCELEHPFLWDKKVSSSTMELSYLEGIA--KSGRPLLIIDAEDEGEALATLVNNMRGTVKIVAVKAPGFDRRKAMILDIAITLTGGVISEE-LGKSLEGATED-LGSAKRVWINKDTT 330
M. avium hsp60 TDAERQEAVLEDPLFLLVSSKVYSTKDLPLPLEKVI--QAGKPLLIIDAEDEGEALSTLVNKLRGFTKSVAVKAPGFDRRKAMILDIAITLGQVISEE-VGLSLESADISL-LGKARKVWVTDETT 329
M. bovis hsp60 TDPERQEAVLEDPLFLLVSSKVYSTKDLPLPLEKVI--GAGKPLLIIDAEDEGEALSTLVNKLRGFTKSVAVKAPGFDRRKAMILDIAITLGQVISEE-VGLTLENADISL-LGKARKVWVTDETT 329
M. leprae groe TDFDSQQAVALDPLVLLHQEKETSSLPLPELPEKVI--ESGKPLLIIDAEDEGEALATLVNSIRTKLKAVAVKSPFFGDRRKAFLEDAIATVGQVWNP-TGLVLRREVGTDV-LGSARRVWVSQDTI 329
M. leprae hsp6 TDAERQEAVLEEPYTLVSSKVYSTKDLPLPLEKVI--QAGKSLIIDAEDEGEALSTLVNKLRGFTKSVAVKAPGFDRRKAMILDIAITLGQVISEE-VGLTLENDSL-LGKARKVWVTDETT 329
M. tuberculosis TDFDNQQAQVLEDALILHQDKISSLPLDPLPLEKVI--GTPKPLLIIDAEDEGEALSTLVNKLRGFTKSVAVKAPGFDRRKAMILDIAITLGQVISEE-VGLSLEKAITLEDD-LGQAKRKEIGKENTT 329
N. meningitidis NDAEKOIAIGLDNPFPVLLFDKKISNFRDPLPLEKVI--KASRPLLIIDAEDEGEALATLVNNTRGKFTIVAVKAPGFDRRKAMILDIAITLGQVISEE-VGLSLEKAITLEDD-LGQAKRKEIGKENTT 331
S. aureus hsp6 TDSDKMVAELEPPLTVDKKISSFODIPLPLEQIV--QSURPILLIIDAEDEGEALATLVNNTRMGTFTAIAVKAPGFDRRKAMILDIAITLGQVISEE-VGLDIKDASIDM-LGTSKVEVTKDNTT 330
Synechocystis TDAERMEAVLEDPLRLLTDKKNLYQDLVPLPLEQIA--RQGKPLLIIDAEDEKEALATLVNNTRGKFTIVAVKAPGFDRRKOMLIEDIAITLGQVISEE-VGLKLESATYDS-LGSARRINITKDNTT 330
Synechocystis TDSRQLVEUNPLPILLTDKKSATAELVPLPLEKVI--RAGRPLLIIDAEDEGEALATLVNNTRGKFTIVAVKAPGFDRRKAVLQDIAITLGQVISEE-VGLSLDTVSLDQ-LGQAVKATLKDNTI 329
Tsukamurella TDAERQEAVLEDPLRLLTDKKSFDIPLPLEKVI--QSGPKLPLIADDEGEALACLNLRGQQLQVIAIKAPGFDRRKAMILDIAITLGQVISEE-TGLQARQVWVTDETT 329
S. pombe hsp60 TDVSKSQKVEFENPLLSEKKVSAQDILPSL-ELAQHQ--RPLPLVIAEDVGEALACLNLRGQQLQVIAIKAPGFDRRKAMILDIAITLGQVISEE-TGLQARQVWVTDETT 362
S. cerevisiae TDPKSSKVEFEKPLLSEKKSSQDILPAL-EISNQS--RPLPLIADDEGEALACLNLRGQQLQVIAIKAPGFDRRKAMILDIAITLGQVISEE-TGLQARQVWVTDETT 352
P. falciparum MN--SQKVUEDKPYLTHEEKKISTVKSLLPYLEHV--LQNOSSLVIAEDVSDALATLVNKLRGKICAVKAPGFGENRKALIHDIAITNGKAYVITEET-GKLKDQPVWSYLGKAKSTINVTDST 358
Onchocerca hs TNNEKMKVILEDPPYLITTEKKLNITIQPLSLTEAVH--KSGKPLLIIDAEDEGEALSTLVNKLRGGLKIVAVKAPGFDRRKEMLEDIAALTNAKYVKDELGKMEDLTLED-LGIAKWKITKDNTT 334
C. elegans hsp TSAKGAKVYEKAIVLLSEKKISQVQDIPAL-ELANKL-RPLPLVIAEDVGEALSTLVNRKLVGLQVIAIKAPGFDRRKAMLDGIAITGASTFGDETDLRI EDITAND-LGEGDEVITIKDNTL 347
D. melanogaster NSSKGAKVYEQDALLLSEKKISQVQDIPAL-LASRTRKPLVIAEDVGEALSTLVNRKLVGLQVIAIKAPGFDRRKAMLDGIAITGASTFGDETDLRI EDITAND-LGEGDEVITIKDNTL 357
human hsp60 NTSGQKCKCQDAYVLLSEKKISQVQDIPAL-EJANAH-RKPLPLVIAEDVGEALSTLVNRKLVGLQVIAIKAPGFDRRKAMLDGIAITGASTFGDETDLRI EDITAND-LGEGDEVITIKDNTL 356
Arabidopsis h TNQKTQKCELDPLPLIHEKKISSINSIVKVL-EALAKR-ORPLLIVSDEVESDALATLINLKLRGKIVCAIKAPGFGENRKANLQDIAITLTGGVISEE-LGMNLKVDLSM-LGTCKKVTVSKDTV 361
maize hsp60 TNSKAQKCFEPDPLIHDPLRKTVMNHAVKVL-EMALKR-ORPLLIVADEVESEALGTLINLKLRGKIVCAIKAPGFGENRKANLQDIAITLTGGVISEE-LGMNLNEPHM-LGSCKKVTVSKDTV 364
RUBISCO chaperone TNPEKSIFFENARVLTIDQKISAIKDIPLLEKTT--QLRAPLITISEDITGEALATLVNKLRGILNVIAIKAPGFGERRKALLQDIAITLTGAEFOASD-LGLLVENTTIEQ-LGLRKVTISKDTT 376

FIG. 10C



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	400	410	420	430	440	450	460	470	480	490	500	510	520
<i>S. pneumoniae</i>	IIDGVGD--AAIAQGRVQAQIQRQIEEST-SDYDREKQLQERLAKLAGGVAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NGGDEATGVNIVLRAALEPLRQIAE												
<i>S. pyogenes</i> hs	IIDGVGD--AAIAQGRVQAQIQRQIEEST-SDYDREKQLQERLAKLAGGVAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NEDONGKIVVALRAMEAPLRLQIVL 456												
<i>S. pneumoniae</i>	IVEGAGN--PEAISHRVWIKSQIETTT-SDFDREKQLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NEDONGKIVVALRAMEAPLRLQIVL 456												
<i>S. pyogenes</i> hs	IVEGAGN--SEANRNTALIJKSQLETTT-SDFDREKQLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-GDEATGRNVIRALLEPVRQIAH 453												
<i>B. subtilis</i> gr	IVEGAGE--TDKTSARVUTQIRAQVEETT-SDFDREKQLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-GDATQGIVNIVIRALEEPVRQIAH 453												
<i>Clostridium h</i>	IVNGRGN--SEEFTKNRVIQOKIQLQEAFTT-SDFDREKQLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-IDEEQGIVNIVIRALEEPVRQIAH 454												
<i>Cowdria</i> hsp60	II-GSVONSCAHQSRCIQJRMQDNST-SDYDKEKLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NDDEQLGIVNIVKRALQAPILKRIK 458												
<i>Haemophilus h</i>	IIDGIGD--EAQIQTGRVQIQRQIEEST-SDYDKEKLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-MEEONGVGIKALRAMEAPL-RQIVA 456												
<i>L. pneumophila</i> 1a	IIDGEKG--ATEINARITQIQRQMEETT-SDYDREKQLQERVAKLAGGVAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NDDNMGINILRRALESPMRQIVT 455												
<i>M. avium</i> hsp60	IVEGAGD--SDA7AGRVAQIRTEENS-SDYDREKQLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-GEETGANTIVRVALERPLQIAF 458												
<i>M. bovis</i> hsp60	IVEGAGD--TDA7AGRVAQIRQETENS-SDYDREKQLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-GDEATGANTIVKVALEPLQIAF 458												
<i>M. leprae</i> groE	IVDGGG--SNDAVAKRVLQRAETEVSD-SEWDREKQLQERVAKLAGGVAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-GDVFGEALKPLWYIAT 455												
<i>M. leprae</i> hsp6	IVEGAGD--TDA7AGRVAQIRTEENS-SDYDREKQLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-GDEATGANTIVKVALEPLQIAF 453												
<i>M. tuberculosis</i>	IVDGGG--TAEAVANRAKHLRAETDKSD-SWDREKQLGERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NDQDAGQIVNIVRATESPLRQIVA 456												
<i>N. meningitidis</i>	IIDGFGD--AAQIQTARVAEIRQQTETAT-SDYDKEKLQERVAKLAGGVAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRARAALLENHTG--NADQDAGQIVNIVRATESPLRQIVA 456												
<i>S. aureus</i> hsp6	VVDGDD--ENSIDARVSOLKSQIEETE-SDFDREKQLQERLAKLSSGGAVIKVGAASESETELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-GDGETGIVNIVLKAUTAPIVRQIAE 454												
<i>Synechocystis</i> IVAEGNE	--AAVKSRCEDIRRQIEETD-SSYDKEKLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-KDEELTGAIIVARALPAPLKRIAE 456												
<i>Synechocystis</i> LVAGADPKRASAGIKERTENIRKEYAASD-SYDKEKIQTRIAKLAGGVAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NDQRVGVNIVLKDACKAPLKQIAE 458													
<i>Tsukamurella</i>	IVDGAGS--KEQ1AGRVSQDIAETENS-SDYDREKQLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-GDEEQGIVNIVKVALDAPVKQIAV 452												
<i>S. pombe</i> hsp60	IMKGAGDH--VKNDRCEOJRGMDPNL1ESEKELQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NFDQKLGVDEVVWD--NFDQKLGVDEVVWD 488												
<i>S. cerevisiae</i>	ILNGSPK--EAQIQTIEKGSDITTTNSYEKEKLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-KLEGVETT--NEDOKLGVEIVRRA.RMPCTIAK 478												
<i>P. falciparum</i>	IMEGEKG--ETINERCEISIRNAKMNT-SDEKEKLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NEDOKIGIEIIRKTLKIPMTIAK 483												
Oncocerca hs	IV-SE-NRVTDVKARIETIKSQIEEST-SDYDKEKLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NDQ1GIVNIVKVALTQPAITVK 472												
<i>C. elegans</i> -hsp	LLRGGRGDQ--TEIEKRTETTDETERST-SDEKEKLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NDQ1GIVNIVKVALTQPAITVK 472												
<i>D. melanogaster</i>	LLKGKGKK--DDVLRANQIRTKIEDTT-SYEKEKLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NDQ1GIVNIVKVALTQPAITVK 481												
human hsp60	LLKGKGDK--AQ1EKRTQETTEQLDVTT-SYEKEKLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NDQ1GIVNIVKVALTQPAITVK 481												
Arabidopsis h	ILDGAGDK--KG1EERCEQIRSATELS-S-YDKEKLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NDQ1GIVNIVKVALTQPAITVK 486												
maize hsp60	ILDGAGDK--KSTEERADQIRSAVENST-S-YDKEKLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NDQ1GIVNIVKVALTQPAITVK 489												
RUBISCO chaperon	IIADAASK--DELQSRVQAKKELSETD-SYDKEKLQERLAKLSSGGAVIKVGAATEVELKERKRVFEDALNATRAAEEGTVPGGGVVALLRAPPALDKLT-E-NDQ1GIVNIVKVALTQPAITVK 503												

FIG. 10D



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NAGLEGSV-VVEKIKN---SEAG-GYNAATGEYVDMIAAGIIDPTKVTRSLQNAASVASLMLTTEAVWDKPEKEAAPAG-MPGM--MGGGGGNGGM--M--									
S. pneumoniae	hs	NCGEEPSV-VANTYKA---	GDGNYGYNAATEEYGNMIDMGILDPLTKVTRSLQYAASVAGLMITTECHNTDLPKGDAPDLG-AAG--GMGGGG						543
S. pyogenes	hs	NAGEEPSV-VTNVYKA---	GEINYGYNAATEEYGNMIDFGILDPLTKVTRSLQYAASVAGLMITTECHNTDLPKGDAPDLG-AAG--MGGGGG						544
S. pneumoniae		NAGFEISI-VIDRJKN---	AELIGFNAATGEWVNMIQDQGLIDPVKVRSLQNAASVASLILTEAVWANKPEVAPAPA-M---DPSMMGGMGG						541
S. pyogenes	hs	NAGYEGSV-VIDKLKN---	SPAGTGFNAATGEWDMIKTGIDIDPKVTRSLQNAASVASLILTEAVWANKPEPATPAPA-MAGMDPGMGGMGG						545
B. subtilis	gr	NAGLEGSV-IVERLKN---	EEIGVGFFNAATGEWVNMIKEGIIDPTKVKTRSLQNAASVAAMFLTTAEVADKPEENGGGAG-NP---DMGGGGGGGGG--M						544
Clostridium	h	NAGLEGSV-IIEKVKN---	SDAGVGFDALRGYEKDMIKAGIVIDPTKVKTRSLQNAASVASFLTTAEAVADIPEK---E-MPQGAGM---GMGGM-Y						539
Cowdria	hsp60	NAGSENAPCVIAHLLKQNDKELI	-FNWDVTFNANAFTSGV1DPLKVRRIAFDFAVSLAAVFMTLNAYWDIPISKDDNSAAGGAGMGGGGGGG-----F						551
Haemophilus	h	NAGEEASV-IASAVKN---	GEINFGYNACTEQYGDIMAGIIDLPTKVKTRSLQFAASVAGLMITTECHNTLPKDKKAIDL-AAGMGGGGGGG--M						547
L. pneumophila	1	NAGYEASV-VVNVKAE---	HKDNYGFNAATGEYGDVMEMGILDPTKVKTRSLQNAASVASLMLTTECHNTDLPKKEEG-VG--GDMGGGGGGGGG--MZ						549
M. avium	hsp60	NGGLEPGV-VAEKVKN---	SPAGTGLNAATGEYEDLKGAGIADPVKVKTRSLQNAASVAGLFLTTEAVADKPEKAAPAG-DPTG-----GMGGMD-----F						541
M. bovis	hsp60	NSGLEPGV-VAEKVKN---	LPAGHGLNAQTGVYEDLLAAGVADPVKVKTRSLQNAASVAGLFLTTEAVADKPEKEAKSVP-G-GG-----DMGGMD-----F						540
M. leprae	groe	NAGLDGAV-VVDKVISG---	LPAGHGLNASTLGYGLVADPVKVKTRSLQNAASVAGMLLTTEAVADKPEKEEEHDH-H-GHAAH						537
M. leprae	hsp6	NSGMEPGV-VAEKVKN	LSVGHGLNATAATGEYEDLLKGAGVADPVKVKTRSLQNAASVAGLFLTTEAVADKPEKTAAPAS-DPTG-----GMGGMD-----F						541
M. tuberculosis	i	NAGLDGSV-VVKKVSE---	LPAGHGLNWTNTSYGLDAADGVIDPVKVKTRSLQNAASVAGLMLTTODCMIAEIPPEKAMPD-HGMMGGGGG--M-----Z						539
N. meningitidis		NAGLEPSV-VVNKVLE---	GKGNYGYNAGSGSEGYGDMIEMGVLDPAKVTRSALQHAASVAGLMLTTODCMIAEIPPEKAMPD-HGMMGGGGG--M-----Z						545
S. aureus	hsp6	NAGLEGSV-IVERLKN---	AEPGVGFNGATNEWVNMLRRGIIDPTKVKTRSLQHAASVAGLMLTTODCMIAEIPPEKAMPD-HGMMGGGGG--M-----Z						539
Synechocystis		NAGQNGAV-ISERVEKE---	KEFINGYNAASLEYVDMLAAGIIVDPAKVTRSALQNAASVAGMLLTTECIVWDKPEKEKAP---A---GAPGGD--FDY						541
Synechocystis		NAGLEGSV-IVEKVKKE---	ATGNGQGYWVITGKIEDLIAGIIDPAKVKTRSLQNAASVAGMLLTTEALYVKEPKPEAAPA---MPDGGMGGGGGGGGG--GMM						552
Tsukamure	11a	NAGLEPSV-VVKKVSE---	SPAGTGLNAATGVYEDLLKGAGIADPVKVKTRSLQNAASSTAALFLTTEAVADKPEKAGAPV--DPTG-----GMGGMD-----F						539
S. pombe	hsp60	NAGLEGNL-IVGKLKELYKEFNIGYDIAKDRFDVLDNEIGVLDPLKVRRTGLVDASGVASLMGTTECAVDAPEESKAPAG-PGM-----GMGGGMGPMM.							583
S. cerevisiae		NAGEEGSV-ITIGKILIDEYGDDFAKGYDASKSEYTDMLATGIDDPFKVVRSGLVDAASVGLLATTEAVIWAPE-PPAAAAGA-GGMP-----GGMPGNPGMM.							573
P. falciparum		NAGHEGSV-VAGN1LKDKNSN1	--GFnAQEGKYVDMIESGILIDPKVKVTAISDAASASLMLTTTEAVIWFDFDSKNEESSO--HMNSVNSMGSMDGGM--Y						577
Oncocerca	hs	NAGLESAV-IIDYLKONNKEI	--YNI-EAMS YANAFAAGVIDPAKVKVRAFETASVAVLTTESMIVDI PNDEN-ASSPMGAGGMGRND-----F						550
C. elegans	hsp	NAGLEPSS-IIDEVIGNSNTSY	--GYDALNGKFVDMFEAGI IDPTKVKWRRTALQDASGVASLLATTCEWTEIPKEEK--GAPAMPGMGGGGGGGGGGGG--MGCGMF						568
D. melanogaster		NAGVDGAM-VVAKVENDAG-DY	--GYDA-KGEYGNLIEKGIDPTKVKWRRTAIDASGVASLLTTAEAVVWTEIPKEEK--D-PGANGAMGGGG--GNGGGMF						576
human	hsp60	NAGVEGSL-IVEKIM-QSSESV-	--GYDAMAGDFVNVMVEKGI IDPTKVKWRRTALQDASGVASLLTTAEAVVWTEIPKEEK--D-PGANGAMGGGG--GNGGGMF						573
Arabidopsis	hs	NAGVEGAV-IVGKILLEQDNPD1	--GYDAAKGEYVDMVKAGI IDPLKVKVTRALVDAASVSSLLTTAEAVVWDLPKDESESGAA-GG-----GMGGMVWMDY						577
maize	hsp60	NAGVEGAV-VVGKILLEQGNTDL	--GYDAAKDEYVDMVKAGI IDPLKVKVTRALVDAASVSSLLMITTIESIIVEIPKEE---AP-----AMGGMGGMDY						576
RUBISCO	chaperone	NAGIEGEV-VVEKIKN---	--GEWEVGYNAMTDYENLVEGVIDPAKVKTRCALQNAASVAGMVLTTQAIWEKPKKAAVAA-APQG-----LTI						587

FIG. 10E



Current Chromatogram(s)

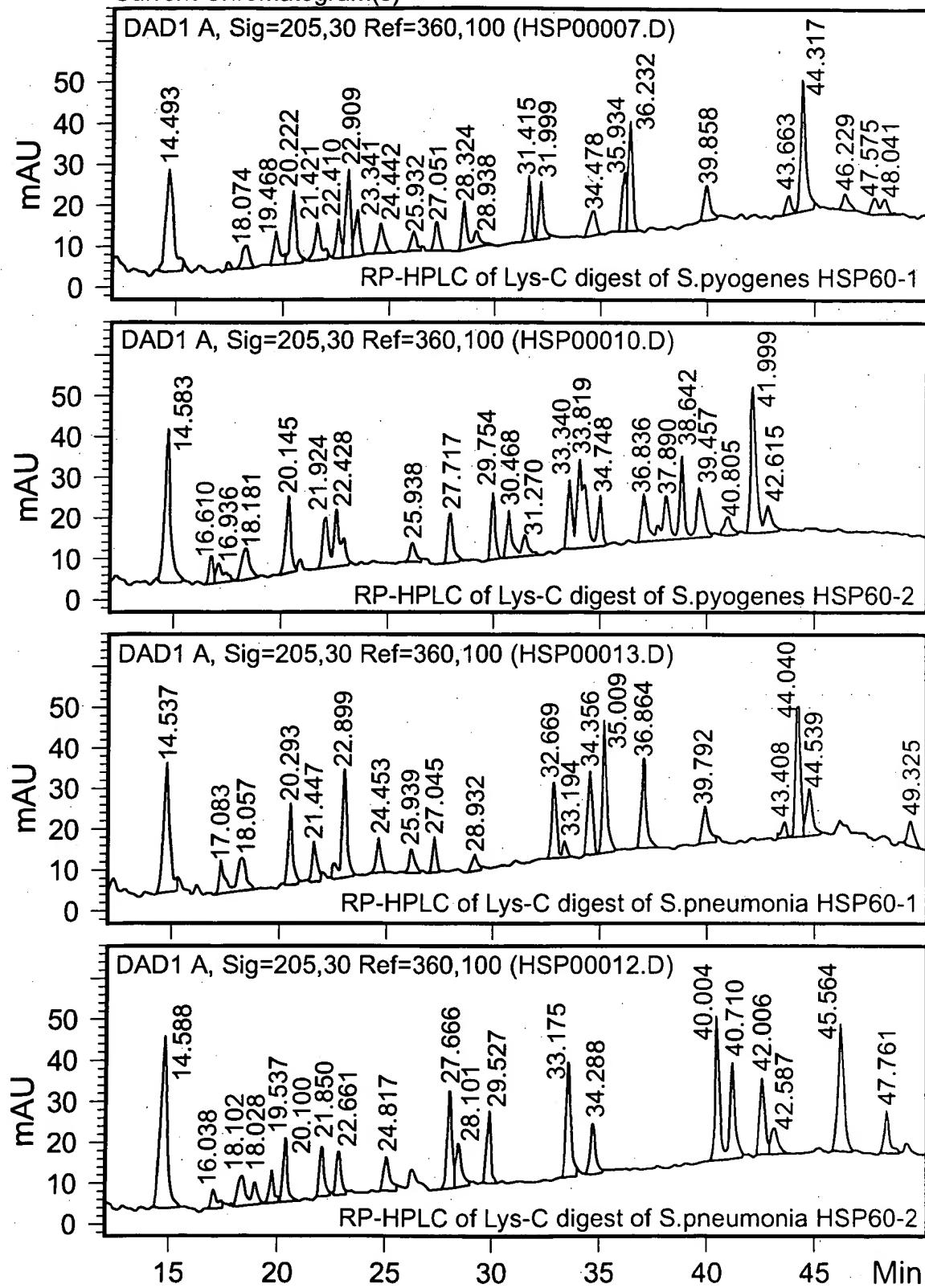


FIG. 11